

OM protein - protein search, using sw model

Run on: March 17, 2003, 16:38:32 ; Search time 19 Seconds
 (without alignments)
 1315.524 Million cell updates/sec

Title: US-09-840-243B-11

Perfect score: 1341

Sequence: 1 MELTQPAEDLIQTOQTQASE.....VIENHILKLFQSNLVPADPE 260

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 9613422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR-73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	219.5	16.4	426	2 AE2149	hypothetical protein
2	214	16.0	2039	2 T15347	hypothetical un
3	207.5	15.5	1031	2 T43458	hypothetical prote
4	202.5	15.1	3924	2 S37431	ankyrin 2, neurona
5	193	14.4	4377	2 A55575	ankyrin 3, long sp
6	189	14.1	1001	2 S30385	G9a protein - huma
7	188.5	14.1	1765	2 T42714	ankyrin 3, splice
8	188.5	14.1	1940	2 T42715	ankyrin 3, splice
9	188.5	14.1	1943	2 T42713	ankyrin 3, splice
10	188.5	14.1	1961	2 T42716	ankyrin 3, splice
11	184	13.7	1881	1 SJHUK	ankyrin 1, erythro
12	183	13.6	1848	2 S37771	ankyrin, erythrocy
13	183	13.6	1862	2 T49502	ankyrin - mouse
14	182	13.6	1856	2 B35049	ankyrin 1, erythro
15	182	13.6	1880	2 A35049	ankyrin 1, erythro
16	181.5	13.5	1549	2 T13940	ankyrin - fruit fl
17	176.5	13.2	2584	2 T24158	hypothetical prote
18	176.5	13.2	2606	2 T24157	hypothetical prote
19	175	13.0	495	2 T27995	hypothetical prote
20	173.5	12.9	888	2 D84650	probable potassium
21	173	12.9	333	2 JC7713	hypothetical prote
22	172.5	12.9	1188	2 T19552	ankyrin-repeat pro
23	171.5	12.8	741	2 A45771	2-5A-dependent RNA
24	171	12.8	1398	2 T21884	hypothetical prote
25	169.5	12.6	1062	2 T14151	Inv protein - mouse
26	167	12.5	211	2 T18174	ankyrin repeat pro
27	166.5	12.4	1062	2 T30255	inversin - mouse
28	166	12.4	658	2 S68418	protein phosphatas
29	165.5	12.3	451	1 S68455	serine/threonine-s

ALIGNMENTS

RESULT 1

AE2149 hypothetical protein **all12748** [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C;Accession: AE2149

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi, S.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.; DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-Fixing Cyanobacterium Anabaena sp. strain PCC 7120

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AE2149

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-426 <KUR>

A;Cross-references: GB:BA000019; PIDN:BAB7447.1; PID:g17131841; GSPDB:GN00179

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all12748

Query Match

Best Local Similarity	Score	DB 2;	Length
30.7%	219.5	2	426;
34	4.6e-10	1	71;
35	1.1e-09	1	35;
4	1.1e-09	1	4;

Matches 62; Conservative 34; Mismatches 71; Indels 35; Gaps 4;

QY 62 QAGSSLIKHSTTL-----TNRQRGNEVSALPATLDSLSIHOLAAQGELDQLK 107
 Db 234 QDGESALHLATVEGYVWDVQVLLNQGANTQIKNKLGDTPLLVAALQGH-----DQIV 285

QY 108 EHLRK-----GDNLVNKPDERGFTPLIWAASFGEIETVRFLLWEWGA
 Db 286 ETLKYGANVHGDNL-----GETPLTLAASQHTATVRLILDYGANANTPASDGKTL 338

QY 162 SLASTGGYTDIVGLLDERDVDINIIYDWNGGTPPLYAVRGNHVKC
 Db 339 IKATERNHPGVIQLLAKGANVNQDOSVGATALLARGADLTTEAD 221

QY 222 SGYTPMDLAVALGYRKVQVIE 243
 Db 399 GGYTALMIAEFGNFRSTIVQILK 420

RESULT 2

T15347 ankyrin-related unc-44 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence_revision 02-Aug-2002

C;Accession: T15347; T15346; T15345; A57282; B57282; C57282

R;Gattung, S.

A;Description: The sequence of *C. elegans* cosmid B0350.

A;Reference number: Z18332

A;Accession: T15347
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 1-2039 <GAT>
 A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208873; PIDN:AAA93443.1
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1000, 'SKLQHRT', 1002-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSAQRS', 1950, 'IVA
 32, 'S', 2034-2035, 'GSPTRSVEEHRHSQHEDHEGST', <GA2>
 A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208875; PIDN:AAA93445.1
 A;Accession: T15344
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1718, 'KW', 1903-1905, 'NRLADESSPS', 1916-1917, 'QRSTIVAAESTSEQVPE', 1934-1935, 'E
 <GA3>
 A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208874; PIDN:AAA93444.1
 A;Accession: T15345
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1718, 'KWEELNRL', 1727, 'D', 'ES', 1942, 'PSAQRS', 1950, 'IVAES', 1956-1957, 'EQVPE
 PTRRSVEEHRHSQHEDHEGST', <GA4>
 A;Cross-references: EMBL:U50071; NID:g1208871; PID:g1208876; PIDN:AAA93446.1
 R;Otsuka, A.J.; Franco, R.; Yang, B.; Shim, K.H.; Tang, L.Z.; Zhang, Y.Y.; Boontrakulpoch
 J. Cell Biol. 129, 1081-1092, 1995
 A;Title: An ankyrin-related gene (unc-44) is necessary for proper axonal guidance in *Cae
 A;Reference number: A57282; MUID:95263663; PMID:7744957
 A;Accession: A57282
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-852, 'GGG', 856-1000, 'SKLQHRT', 1002-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWE
 'SHRED', 2007-2008, 'TI', 2011, 2017, 'TT', 2020-2022, 'SHIS' <OTS>
 A;Cross-references: GB:U21734; NID:g790607; PIDN:AAA85854.1; PID:g790608
 A;Accession: B57282
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 831-852, 'GGG', 856-1319, 'IG', 1322-1595, 'DA', 1598-1718, 'KWEELNRL', 1727, 1799, 'E
 V', 1945-1947, 'VT', 1950, 'SH', 1975, 'SESP', 1980-1981, 'SPTRRSVEEHRHS', 1984-1985, 'EDHEGS', 1
 A;Cross-references: GB:U21731
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 194, 'F', 196, 'I', 198, 'DC', 201, 'G', 409, 'AV', 412, 'Q', 414, '824', 'S', 826, 'ER', 829,
 4, 'TIV', 1828, 'ESTS', 1833, 'QV', 1836, 'E', 1934-1935, 'EQS', 1939, 'ESES', 1944, 'REDDGTIVTT', 194
 A;Cross-references: GB:U21732; NID:g790603; PIDN:AAA85853.1; PID:g790604
 C;Genetics:
 A;Gene: CESP:unc-44
 A;Introns: 97/3; 262/2; 535/1; 749/1; 786/3; 883/3; 1001/2; 1045/3; 1660/1; 1719/2; 1979
 C;Supertfamily: ankyrin; ankyrin repeat homology <AN04>
 F;164-192/Domain: ankyrin repeat homology <AN1>
 F;358-390/Domain: ankyrin repeat homology <AN11>
 F;391-423/Domain: ankyrin repeat homology <AN11>
 Query Match 16.0%; Score 214; DB 2; Length 2039;
 Best Local Similarity 27.3%; Pred. No. 1.2e-08; Mismatches 87; Indels 42; Gaps 4;
 Matches 62; Conservative 36; Mismatches 87; Indels 42; Gaps 4;
 QY 19 SELGDPEDPGEAAADGSSDTWVLSLFPCTPEPVNPERPDAVASVSSPQAGSSLKHSTTLNRQR 78
 Db 2 SNEGDPQQQQQQPESQEVQA---PAAPEPGRAE----- 32
 QY 79 GNEVALPATLDLSIHQHOLAQGELDQLKEHLRGKDNLVNKPDERGFTPLIWASAFGEIB 138
 Db 33 -----GSASFLLRAARAGDLEKVELLRAGTD-INTSNANGLNLHLASKEGHSE 80
 QY 139 TVRFELLEWGADPHILAKERESALSLASTGGYTDIVGLLERDVINLYDWNGGTPLLYAV 198
 Db 81 VVRELIKRQAQDAATRKGNTALHIAASLAGQSLIVTIVENGANVNVQSVNGFTPLYMAA 140
 QY 199 RGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGY-RKQQVIE 244
 Db 141 QENHEEVVKYLLKHGQANQALSTEDGFTPLAVALQQGHDRWVAVLEN 187*

RESULT 3
 T43458
 hypothetical protein DKFZp434F0621.1 - human
 C;Species: Homo sapiens (man)
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000
 C;Accession: T43458
 R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 A;Reference number: Z22517
 A;Accession: T43458
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1031 <AAA>
 A;Cross-references: EMBL:AL133620
 A;Experimental source: adult testis; clone DKFZp434F0621
 C;Genetics:
 A;Note: DKFZp434F0621.1

Query Match 15.5%; Score 207.5; DB 2; Length 1031;
 Best Local Similarity 34.5%; Pred. No. 1.5e-08;
 Matches 51; Conservative 34; Mismatches 60; Indels 3; Gaps 3;
 QY 100 QGELDQLKEHLRKGDNLVNKPDERGFTPLIWASAFGEIETVRFLLEWGA
 Db 81 EGHVHIVEELLIKCGVNLLEHR-DMGGWTALMWACYKGR
 TDVELLLSHGANGPSVTLQYSV 139
 QY 160 ALSLASTG-GYTDIVGLLERDV
 Db 140 YPIIWAAGRGHADIVHILLQNGAKVNCSDKYTTPLVWAARKGH
 LEVCKHLLAMGADVQ 199
 QY 219 EADSGYTPMDLAVALGY-RKVQVQV
 Db 200 EGANSMTALIVAVKGGYTQSVKEILKR 227

RESULT 4
 S37431
 ankyrin 2, neuronal long splice form - human
 N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
 N;Contains: ankyrin 2, short form
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 13-Aug-1999
 C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
 R;Chan, W.
 submitted to the EMBL Data Library, September 1993
 A;Reference number: S37431
 A;Accession: S37431
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-3924 <CHA>
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288
 R;Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.
 J. Cell Biol. 114, 241-253, 1991
 A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal a
 A;Reference number: A39643; MUID:91302466; PMID:1830053
 A;Accession: A39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-2077 <OT1>
 A;Cross-references: GB:X56957
 A;Accession: B39643
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1443, 3585-3924 <OT2>
 A;Cross-references: EMBL:X56958
 R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Ward,
 Genomics 10, 858-866, 1991
 A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
 A;Reference number: A40334
 A;Accession: A40334
 A;Molecule type: DNA
 A;Residues: 463-474, 'PE', 477-495 <TS>

A;Cross-references: GB: M37123; NID: g178647; PIDN: AAA62828.1; PID: g178648
 R;Chan, W.; Kordeli, E.; Bennett, V.
 J. Cell Biol. 123, 1463-1473, 1993

A;Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and se
 A;Reference number: A49462; MUID: 94075409; PMID: 8253844

A;Accession: A49462
 A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA
 A;Residues: 1-3924 <RES>
 A;Cross-references: EMBL: Z26634; NID: g406287; PIDN: CAA81387.1; PID: g406288
 A;Cross-references: C:Genetics:
 A;Gene: GDB: ANK2
 A;Cross-references: GDB: 127607; OMIM: 106410
 A;Map position: 4q25-4q27
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing
 F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>
 F;2-3924/Product: ankyrin 2, short form #status predicted <MA2>
 F;63-95/Domain: ankyrin repeat homology <AN01>
 F;129-161/Domain: ankyrin repeat homology <AN02>
 F;162-190/Domain: ankyrin repeat homology <AN03>
 F;191-223/Domain: ankyrin repeat homology <AN04>
 F;232-264/Domain: ankyrin repeat homology <AN05>
 F;265-297/Domain: ankyrin repeat homology <AN06>
 F;298-330/Domain: ankyrin repeat homology <AN07>
 F;331-363/Domain: ankyrin repeat homology <AN08>
 F;364-396/Domain: ankyrin repeat homology <AN09>
 F;397-429/Domain: ankyrin repeat homology <AN10>
 F;430-462/Domain: ankyrin repeat homology <AN11>
 F;465-497/Domain: ankyrin repeat homology <AN12>
 F;498-530/Domain: ankyrin repeat homology <AN13>
 F;531-563/Domain: ankyrin repeat homology <AN14>
 F;564-596/Domain: ankyrin repeat homology <AN15>
 F;597-629/Domain: ankyrin repeat homology <AN16>
 F;630-662/Domain: ankyrin repeat homology <AN17>
 F;663-695/Domain: ankyrin repeat homology <AN18>
 F;696-728/Domain: ankyrin repeat homology <AN19>
 F;729-761/Domain: ankyrin repeat homology <AN20>
 F;562-594/Domain: ankyrin repeat homology <AN21>
 F;595-627/Domain: ankyrin repeat homology <AN22>
 F;628-660/Domain: ankyrin repeat homology <AN23>
 F;661-693/Domain: ankyrin repeat homology <AN24>
 F;727-759/Domain: ankyrin repeat homology <AN25>
 F;760-792/Domain: ankyrin repeat homology <AN26>
 F;793-825/Domain: ankyrin repeat homology <AN27>

Query Match 15.1%; Score 202.5; DB 2; Length 3924;
 Best Local Similarity 29.3%; Pred. No. 2.6e-07;
 Matches 56; Conservative 43; Mismatches 81; Indels 11; Gaps 4;

QY 55 DASVSSPQAGSSLKHTTLLNRQNGNEVSALPATLDLSIHLQAQGELDQQLKEHLRKGD 114
 Db 5 DAAQKS-DSGEKFNGSSQRKRKKSDSNA-----SFLRAARAGNLDKVEYLKGII 55

QY 115 NLVNPDERGFTPLIWAASFGEIETVRFLEWGADPHILAKERESALSLASTGGYDIVG 174
 Db 56 D-INTCNQNLNLHAAKEGHVGLVQELLGRGSSVDSATKKGNLTALHIAASLAGQAEVK 114

QY 175 LLERDVDINIYDWNGGTPPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALG 234
 Db 115 VLVKEGANINAQSONGFTPLYMAAQENHIDVVKYLLENGANQSTATEDGFTPLAVALQQ 174

QY 235 YRK-VQQVIE 244
 Db 175 HNQAVAILLEN 185

RESULT 5
 A55575
 ankyrin 3, long splice form - human
 N;Alternate names: ankyrin G
 C;Species: Homo sapiens (man)
 C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 20-Sep-1999
 C;Accession: A55575
 R;Kordeli, E.; Lambert, S.; Bennett, V.
 J. Biol. Chem. 270, 2352-2359, 1995
 A;Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax

A;Reference number: A55575; MUID: 95138209; PMID: 7836469
 A;Accession: A55575
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-4377 <KOR>
 A;Cross-references: GB: U13616; NID: g608024; PIDN: AAA64834.1; PID: 9608025
 A;Cross-references: C:Genetics:
 A;Gene: GDB: ANK3
 A;Cross-references: GDB: 424503; OMIM: 600465
 A;Map position: 10q21-10q21
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 C;Keywords: alternative splicing; peripheral membrane protein
 F;73-105/Domain: ankyrin repeat homology <AN01>
 F;106-138/Domain: ankyrin repeat homology <AN02>
 F;139-171/Domain: ankyrin repeat homology <AN03>
 F;172-200/Domain: ankyrin repeat homology <AN04>
 F;201-233/Domain: ankyrin repeat homology <AN05>
 F;234-266/Domain: ankyrin repeat homology <AN06>
 F;267-299/Domain: ankyrin repeat homology <AN07>
 F;300-332/Domain: ankyrin repeat homology <AN08>
 F;333-365/Domain: ankyrin repeat homology <AN09>
 F;366-398/Domain: ankyrin repeat homology <AN10>
 F;399-431/Domain: ankyrin repeat homology <AN11>
 F;432-464/Domain: ankyrin repeat homology <AN12>
 F;465-497/Domain: ankyrin repeat homology <AN13>
 F;498-530/Domain: ankyrin repeat homology <AN14>
 F;531-563/Domain: ankyrin repeat homology <AN15>
 F;564-596/Domain: ankyrin repeat homology <AN16>
 F;597-629/Domain: ankyrin repeat homology <AN17>
 F;630-662/Domain: ankyrin repeat homology <AN18>
 F;663-695/Domain: ankyrin repeat homology <AN19>
 F;696-728/Domain: ankyrin repeat homology <AN20>
 F;729-761/Domain: ankyrin repeat homology <AN21>
 F;762-794/Domain: ankyrin repeat homology <AN22>
 F;795-827/Domain: ankyrin repeat homology <AN23>

Query Match 14.4%; Score 193; DB 2; Length 4377;
 Best Local Similarity 28.1%; Pred. No. 1.8e-06;
 Matches 50; Conservative 43; Mismatches 75; Indels 10; Gaps 3;

QY 68 KHSTTLNRQNGNEVSALPATLDLSIHLQAQGELDQQLKEHLRKGDNLVNPDPDERGFTP 127
 Db 27 KHRKRSRDRKKSDANA-----SYLRAARAGHLEKALDYIKNGVD-INICQNGLNA 77

QY 128 LIWASAFGEIETVRFLEWGADPHILAKERESALSLASTGGYDIVGLLERDVDDINYD 187
 Db 78 LHLASKEGHVEVSELLQREANVDAATKKGNLTALHIAASLAGQAEVKVVLVTNGANVNAQS 137

QY 188 WNGGTPPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGY-RKVQQVIE 244
 Db 138 QNGFTPLYMAAQENHLEVKFLLDNGASQSLATEDGFTPLAVALQQGHDQVVSLLEN 195

RESULT 6
 S30385
 G9a protein - human
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C;Accession: S30385
 R;Milner, C.M.; Campbell, R.D.
 Biochem. J. 290, 811-818, 1993
 A;Title: The G9a gene in the human major histocompatibility complex encodes a novel prot
 A;Reference number: S30385; MUID: 93207535; PMID: 8457211
 A;Accession: S30385
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1001 <ML>
 A;Cross-references: EMBL: X69838; NID: g287864; PIDN: CAA49491.1; PID: g287865
 C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
 F;641-673/Domain: ankyrin repeat homology <ANR>

Query Match 14.1%; Score 189; DB 2; Length 1001;
 Best Local Similarity 35.3%; Pred. No. 4.6e-07;

Matches 49; Conservative 18; Mismatches 72; Indels 0; Gaps 0;

QY 91 SLSIHOLAAQGELDQDILKEHLRKGDNLVNPDPERGFTPLIWAQAFGEIETVRFLEWGADP 150
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42715
 Db 543 STCLHHAAKIGNLEMWSSLSTGQDQVNAQDSSGGWTPITWAEEHKHIEVIRMLTRGADV 602
 QY 151 HILAKERESALSLASTGGYTDIVGLLERDWDNIVYDWNNGTPLLYAVRGHVKCVEAHL 210
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42715
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A;Residues: 1-1940 <PET>
 A;Cross-references: EMBL:L40632; NID:9710548; PID:9710549; PIDN:AAB01604.1
 A;Experimental source: strain C57BL/6J; kidney
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 834/1
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing

RESULT 7

T42714
 ankyrin 3, splice form 2 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42714
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A;Residues: 1-1765 <PET>
 A;Accession: T42714
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-1765 <PET>
 A;Cross-references: EMBL:L40632; NID:9710548; PID:9710551; PIDN:AAB01605.1
 A;Experimental source: strain C57BL/6J; kidney
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 1587/1
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing

Query Match 14.1%; Score 188.5; DB 2; Length 1940;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06; Indels 61; Gaps 6;
 Matches 62; Conservative 43; Mismatches 77; Gaps 6;

QY 62 QAGSSLKHSTT-----LTNRQRGNEVSALPATLD---SLSI-----HQLAAQGE 102
 Db 503 QQGASPNAATTSGYTPPLHAAREGHEDVAAF--LLDHGASLSITTKKGFTPLHVAAKYKG 560
 QY 103 LDQLKEHLRKGDNLVNPDP-----ERGFT 126
 Db 561 LEVASLLLQKSAS---PDAAGKSGLTPHLVAHYDNQKVALLLQGASPHAAKNGYT 616
 QY 127 PLIWAQAFGEIETVRFLEWGADPHILAKERESALSLASTGGYTDIVGLLERDWDNIVY 186
 Db 617 PLHIAAKKNQMDIATSLLEYGADANAVTROQIASVHLAAQEGHVDMVSLLSRNANVNL 676
 QY 187 DWNGGTPLLYAVRGHVKCVEAHLARGADLTTEADSGYTPMDLAVALGYRKVQQVIEHT 246
 Db 677 NRSGLTPHLAAQEDRVNVVAEVLVNQGAHVDAQTKMGYTPHLHVGCHYGNIKIVNFLQHS 736
 QY 247 LKL 249
 Db 737 ARV 739

Query Match 14.1%; Score 188.5; DB 2; Length 1765;
 Best Local Similarity 25.5%; Pred. No. 1.1e-06; Indels 61; Gaps 6;
 Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSSLKHSTT-----LTNRQRGNEVSALPATLD---SLSI-----HQLAAQGE 102
 Db 503 QQGASPNAATTSGYTPPLHAAREGHEDVAAF--LLDHGASLSITTKKGFTPLHVAAKYKG 560
 QY 103 LDQLKEHLRKGDNLVNPDP-----ERGFT 126
 Db 561 LEVASLLLQKSAS---PDAAGKSGLTPHLVAHYDNQKVALLLQGASPHAAKNGYT 616
 QY 127 PLIWAQAFGEIETVRFLEWGADPHILAKERESALSLASTGGYTDIVGLLERDWDNIVY 186
 Db 617 PLHIAAKKNQMDIATSLLEYGADANAVTROQIASVHLAAQEGHVDMVSLLSRNANVNL 676
 QY 187 DWNGGTPLLYAVRGHVKCVEAHLARGADLTTEADSGYTPMDLAVALGYRKVQQVIEHT 246
 Db 677 NRSGLTPHLAAQEDRVNVVAEVLVNQGAHVDAQTKMGYTPHLHVGCHYGNIKIVNFLQHS 736
 QY 247 LKL 249
 Db 737 ARV 739

RESULT 8

T42715
 ankyrin 3, splice form 3 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42715
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A;Residues: 1-1943 <PET>
 A;Cross-references: EMBL:L40632; NID:9710548; PID:9710550; PIDN:AAB01606.1
 A;Experimental source: strain C57BL/6J; kidney
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 855/1
 C;Function:
 A;Description: supposed to play an important role in the polarized distribution of many
 C;Keywords: ankyrin; ankyrin repeat homology

RESULT 9

T42713
 ankyrin 3, splice form 1 - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
 C;Accession: T42713
 R;Peters, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Vialamas, M.; Turtzo, I.
 J. Cell Biol. 130, 313-330, 1995
 A;Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
 the repeat domain.
 A;Residues: 1-1943 <PET>
 A;Cross-references: EMBL:L40632; NID:9710548; PID:9710550; PIDN:AAB01606.1
 A;Experimental source: strain C57BL/6J; kidney
 C;Genetics:
 A;Gene: Ank3
 A;Map position: 10
 A;Introns: 855/1
 C;Function:
 A;Description: major kidney ankyrin
 C;Keywords: ankyrin; ankyrin repeat homology

Query Match 14.1%; Score 188.5; DB 2; Length 1943;
 Best Local Similarity 25.5%; Pred. No. 1.3e-06; Indels 61; Gaps 6;
 Matches 62; Conservative 43; Mismatches 77; Indels 61; Gaps 6;

QY 62 QAGSSLKHSTT-----LTNRQRGNEVSALPATLD---SLSI-----HQLAAQGE 102

Db 503 QQGASPNATTSGYTPHLAAAREGHEDVAAF--LLDHGASLSITKKGGTPHLVAALKYKG 560
 C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
 C; Accession: S08275; PC2220; A35443
 R; Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990
 A; Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
 A; Reference number: S08275; MUID:90158830; PMID:2137557
 A; Accession: S08275
 A; Molecule type: mRNA
 A; Residues: 1-1881 <LUI1>
 A; Cross-references: EMBL:X16609; NID:928701; PIDN:CAA34610.1; PID:g28702
 A; Accession: A33219
 A; Molecule type: protein
 A; Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30; 733-749, 'A', 751-753; 828-833, 'X', 835-855, 'X'
 X', 1367-1383-1427; 1601-1630; 1686-1698, 'D', 1700-1763-1772 <LUK>
 A; Note: 845-Arg and 1392-Thr were also found
 R; Hermann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994
 A; Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
 A; Reference number: PC2220; MUID:95071348; PMID:7526850
 A; Accession: PC2220
 A; Molecule type: protein
 A; Residues: 910-929 <HER>
 R; Davis, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A; Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
 A; Reference number: A35443; MUID:90285190; PMID:2141335
 A; Accession: A35443
 A; Molecule type: protein
 A; Residues: 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'LQ'; 797-800, 'L', 802-814; 862-863,
 C; Genetics:
 A; Gene: GDB:ANK1; ANK
 A; Cross-references: GDB:118737; OMIM:182900
 A; Map position: 8p11.2-8p11.2
 C; Superfamily: ankyrin; ankyrin repeat homology
 C; Keywords: alternative splicing; phosphoprotein
 F; 2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
 F; 2-1512, 1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
 F; 2-827/Domain: 89K #status predicted <DOM1>
 F; 44-76/Domain: anion exchange protein binding
 F; 77-109/Domain: ankyrin repeat homology <AN01>
 F; 110-142/Domain: ankyrin repeat homology <AN02>
 F; 143-171/Domain: ankyrin repeat homology <AN03>
 F; 172-204/Domain: ankyrin repeat homology <AN05>
 F; 205-237/Domain: ankyrin repeat homology <AN06>
 F; 238-270/Domain: ankyrin repeat homology <AN07>
 F; 271-303/Domain: ankyrin repeat homology <AN08>
 F; 304-336/Domain: ankyrin repeat homology <AN09>
 F; 337-369/Domain: ankyrin repeat homology <AN10>
 F; 370-402/Domain: ankyrin repeat homology <AN11>
 F; 403-435/Domain: ankyrin repeat homology <AN12>
 F; 436-468/Domain: ankyrin repeat homology <AN13>
 F; 469-501/Domain: ankyrin repeat homology <AN14>
 F; 502-534/Domain: ankyrin repeat homology <AN15>
 F; 535-567/Domain: ankyrin repeat homology <AN16>
 F; 568-600/Domain: ankyrin repeat homology <AN17>
 F; 601-633/Domain: ankyrin repeat homology <AN18>
 F; 634-666/Domain: ankyrin repeat homology <AN19>
 F; 667-699/Domain: ankyrin repeat homology <AN20>
 F; 700-732/Domain: ankyrin repeat homology <AN21>
 F; 733-765/Domain: ankyrin repeat homology <AN22>
 F; 766-798/Domain: ankyrin repeat homology <AN23>
 F; 828-1382/Domain: 62K #status predicted <DOM2>
 F; 828-1382/Region: spectrin binding
 F; 1383-1881/Domain: 55K #status predicted <DOM3>

RESULT 11
 SJHJK
 ankyrin 1, erythrocyte splice form 1 - human
 N; Alternative names: ankyrin 2.1, erythrocyte; ankyrin-R
 N; Contains: ankyrin 2.2
 C; Species: Homo sapiens (man)

Query Match 13.7%; Score 184; DB 1; Length 1881;
 Best Local Similarity 23.1%; Pred. No. 2.9e-06;
 Matches 54; Conservative 37; Mismatches 69; Indels 74; Gaps 3;

Db 617 PLIWAQKQMDIATSLLEYGADANAVTRQGIAVHLAAQEGHVDMSLLSRNANVNL 676
 C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
 C; Accession: S08275; PC2220; A35443
 R; Lux, S.E.; John, K.M.; Bennett, V.
 Nature 344, 36-42, 1990
 A; Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure
 A; Reference number: S08275; MUID:90158830; PMID:2137557
 A; Accession: S08275
 A; Molecule type: mRNA
 A; Residues: 1-1881 <LUI1>
 A; Cross-references: EMBL:X16609; NID:928701; PIDN:CAA34610.1; PID:g28702
 A; Accession: A33219
 A; Molecule type: protein
 A; Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30; 733-749, 'A', 751-753; 828-833, 'X', 835-855, 'X'
 X', 1367-1383-1427; 1601-1630; 1686-1698, 'D', 1700-1763-1772 <LUK>
 A; Note: 845-Arg and 1392-Thr were also found
 R; Hermann, J.; Barel, M.; Frade, R.
 Biochem. Biophys. Res. Commun. 204, 453-460, 1994
 A; Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane
 A; Reference number: PC2220; MUID:95071348; PMID:7526850
 A; Accession: PC2220
 A; Molecule type: protein
 A; Residues: 910-929 <HER>
 R; Davis, L.H.; Bennett, V.
 J. Biol. Chem. 265, 10589-10596, 1990
 A; Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger
 A; Reference number: A35443; MUID:90285190; PMID:2141335
 A; Accession: A35443
 A; Molecule type: protein
 A; Residues: 'X', 5, 'X', 7-12; 403-417, 'X', 419-422, 'H', 424, 'LQ'; 797-800, 'L', 802-814; 862-863,
 C; Genetics:
 A; Gene: GDB:ANK1; ANK
 A; Cross-references: GDB:118737; OMIM:182900
 A; Map position: 8p11.2-8p11.2
 C; Superfamily: ankyrin; ankyrin repeat homology
 C; Keywords: alternative splicing; phosphoprotein
 F; 2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>
 F; 2-1512, 1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>
 F; 2-827/Domain: 89K #status predicted <DOM1>
 F; 44-76/Domain: anion exchange protein binding
 F; 77-109/Domain: ankyrin repeat homology <AN01>
 F; 110-142/Domain: ankyrin repeat homology <AN02>
 F; 143-171/Domain: ankyrin repeat homology <AN03>
 F; 172-204/Domain: ankyrin repeat homology <AN05>
 F; 205-237/Domain: ankyrin repeat homology <AN06>
 F; 238-270/Domain: ankyrin repeat homology <AN07>
 F; 271-303/Domain: ankyrin repeat homology <AN08>
 F; 304-336/Domain: ankyrin repeat homology <AN09>
 F; 337-369/Domain: ankyrin repeat homology <AN10>
 F; 370-402/Domain: ankyrin repeat homology <AN11>
 F; 403-435/Domain: ankyrin repeat homology <AN12>
 F; 436-468/Domain: ankyrin repeat homology <AN13>
 F; 469-501/Domain: ankyrin repeat homology <AN14>
 F; 502-534/Domain: ankyrin repeat homology <AN15>
 F; 535-567/Domain: ankyrin repeat homology <AN16>
 F; 568-600/Domain: ankyrin repeat homology <AN17>
 F; 601-633/Domain: ankyrin repeat homology <AN18>
 F; 634-666/Domain: ankyrin repeat homology <AN19>
 F; 667-699/Domain: ankyrin repeat homology <AN20>
 F; 700-732/Domain: ankyrin repeat homology <AN21>
 F; 733-765/Domain: ankyrin repeat homology <AN22>
 F; 766-798/Domain: ankyrin repeat homology <AN23>
 F; 828-1382/Domain: 62K #status predicted <DOM2>
 F; 828-1382/Region: spectrin binding
 F; 1383-1881/Domain: 55K #status predicted <DOM3>

RESULT 11
 SJHJK
 ankyrin 1, erythrocyte splice form 1 - human
 N; Alternative names: ankyrin 2.1, erythrocyte; ankyrin-R
 N; Contains: ankyrin 2.2
 C; Species: Homo sapiens (man)

Query Match 74 TNRQRGNEWSALPATLDSLISIHQIAQGELDQLKEHLRKGDNLVNPDPDERGFTPLIWASA 133
 Db 73 TTTKGN---TALHIALAGQDEVRELVNYGAN-VNAQSOKGFTPLYMAQ 120

Db 245 TPLHIASRRGNVIMVRLLDRGQAQIERTKDELTPLHCARNGHVRISEILLDH 298

QY 134 FGEIETVRFLEWGADPHILAKERESALSLASTGGYTDIVG----- 174

Db 121 ENHLEVVKFLENGANQNVATEDGFTPLAVALQOQHENVV AHLINYGTKGKVR LPALHIA 180

QY 175 -----LLERD D V D I N I Y D W N G G 191

Db 181 ARNDDDTRTAAVLLQNDPNPDVLSKIGFTPLHIAAHYENLNVAQQLLN RGA SVNFTPQNGI 240

QY 192 TPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKVQVIE NH 245

Db 241 TPLHIASRRGNVIMVRLLDRGQAQIERTKDELTPLHCARNGHVRISEILLDH 294

RESULT 12

S3771

ankyrin, erythrocyte - mouse

C;Species: Mus musculus (house mouse)

C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999

C;Accession: S3771

R;Birkenmeier, C.S.; White, R.A.; Peters, L.L.; Hall, E.J.; Lux, S.E.; Barker, J.E.

J;Biol. Chem. 268, 9533-9540, 1993

A;Title: Complex patterns of sequence variation and multiple 5' and 3' ends are found at

A;Reference number: S3771; MUID:93252825; PMID:8486643

A;Accession: S3771

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1848 <BIR>

A;Cross-references: EMBL:X69063; NID:g311816; PIDN:CAA48801.1; PID:g311817

C;Superfamily: ankyrin; ankyrin repeat homology

C;Keywords: alternative splicing

F;48-80/Domain: ankyrin repeat homology <AN01>

F;81-113/Domain: ankyrin repeat homology <AN02>

F;114-146/Domain: ankyrin repeat homology <AN03>

F;147-175/Domain: ankyrin repeat homology <AN04>

F;176-208/Domain: ankyrin repeat homology <AN05>

F;209-241/Domain: ankyrin repeat homology <AN06>

F;242-274/Domain: ankyrin repeat homology <AN07>

F;275-307/Domain: ankyrin repeat homology <AN08>

F;308-340/Domain: ankyrin repeat homology <AN09>

F;341-373/Domain: ankyrin repeat homology <AN10>

F;374-406/Domain: ankyrin repeat homology <AN11>

F;407-439/Domain: ankyrin repeat homology <AN12>

F;440-472/Domain: ankyrin repeat homology <AN13>

F;506-538/Domain: ankyrin repeat homology <AN14>

F;539-571/Domain: ankyrin repeat homology <AN15>

F;572-604/Domain: ankyrin repeat homology <AN16>

F;605-637/Domain: ankyrin repeat homology <AN18>

F;638-670/Domain: ankyrin repeat homology <AN19>

F;671-703/Domain: ankyrin repeat homology <AN20>

F;704-736/Domain: ankyrin repeat homology <AN21>

F;737-769/Domain: ankyrin repeat homology <AN22>

F;770-802/Domain: ankyrin repeat homology <AN23>

Query Match

Best Local Similarity 13.6%; Score 183; DB 2; Length 1848;

Matches 54; Conservative 36; Mismatches 70; Indels 74; Gaps 3;

QY 74 TNRQRGNEWSALPATLDSL SIHQLAAQGELDQI KEHLRKGDNLV NKPD ERGFTPLI WASA 133

Db 69 TTTKGN-----TALHAA LAGQDEVV RELV NYGAN-VNAQS QKGFT PLYMAQ 116

QY 134 FGEIETVRFLEWGADPHILAKERESALSLASTGGYTDIVG----- 174

Db 117 ENHLEVVKFLENGANQNVATEDGFTPLAVALQOQHENVV AHLINYGTKGKVR LPALHIA 176

QY 175 -----LLERD D V D I N I Y D W N G G 191

Db 177 ARNDDDTRTAAVLLQNDPNPDVLSKIGFTPLHIAAHYENLNVAQQLLN RGA SVNFTPQNGI 236

QY 192 TPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKVQVIE NH 245

Db 237 TPLHIASRRGNVIMVRLLDRGQAQIERTKDELTPLHCARNGHVRISEILLDH 290

RESULT 14

B35049

ankyrin 1, erythrocyte splice form 3 - human

N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N;Contains: ankyrin 2.2, erythrocyte

C;Species: Homo sapiens (man)

C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
 C;Accession: B35049
 R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 A;Title: cDNA sequence for human erythrocyte ankyrin.
 A;Reference number: A35049; MUID:90175370; PMID:1689849
 A;Accession: B35049
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1880 <LAM>
 A;Cross-references: GB:M288830
 C;Genetics:
 A;Gene: GDB:ANK1; ANK
 A;Cross-references: GDB:118737; OMIM:182900
 A;Map position: 8p11.2-8p11.2
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing
 F;2-1856/Product: ankyrin 1, erythrocyte form 3 #status predicted <MAT>
 F;2-1513, 1676-1856/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;44-76/Domain: ankyrin repeat homology <AN01>
 F;77-109/Domain: ankyrin repeat homology <AN02>
 F;110-142/Domain: ankyrin repeat homology <AN03>
 F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN13>
 F;469-501/Domain: ankyrin repeat homology <AN14>
 F;502-534/Domain: ankyrin repeat homology <AN15>
 F;535-567/Domain: ankyrin repeat homology <AN16>
 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-699/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>
 F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>
 Query Match 13.6%; Score 182; DB 2; Length 1856;
 Best Local Similarity 26.4%; Pred. No. 4.1e-06;
 Matches 61; Conservative 34; Mismatches 135; Indels 1; Gaps 1;
 Qy 8 EDLIQTOQTASELGDPEPDGEEAADGSDTIVVLSLFPCTPEPVNPEDDASVSSPQAGSSL 67
 Db 421 KNLLQRGASPNSNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKDDQTPHLCAARI 480
 Qy 68 KHSTTLNRQRGNEVSALPATLDSLISIHQLAQGELDQLKEHLRKGDNLVNKPDERGFTP 127
 Db 481 GHTNMVKLLENNANPNLATAGHTPLHIAAREGHVETVALLKEASQACM-TKKGFTP 539
 Qy 128 LIWASAFGEIETVRFLEWGADPHILAKERESALSLASTGGYDIVGLLDERDVNDINYD 187
 Db 540 LHVAKYKGKVRVAELLERDAHPNAAGKNGLTPLHVAVHHNNLDIVKULLPRGGSPHSPA 599
 Qy 188 WNGGTPPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKV 238
 Db 600 WNGGTPPLHYAKQNOVEVARSLLQYGGSSANAESVQGVTPHLAAQEGHAEM 650
 A35049
 ankyrin 1, erythrocyte splice form 2 - human
 N;Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R
 N;Contains: ankyrin 2.2, erythrocyte
 C;Species: Homo sapiens (man)
 C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
 C;Accession: A35049
 R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; K
 Proc. Natl. Acad. Sci. U.S.A. 87, 1730-1734, 1990
 RESULT 15
 A35049
 A;Title: cDNA sequence for human erythrocyte ankyrin.
 A;Reference number: A35049; MUID:90175370; PMID:1689849
 A;Accession: A35049
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1880 <LAM>
 A;Cross-references: GB:118737; OMIM:182900
 A;Map position: 8p11.2-8p11.2
 C;Superfamily: ankyrin; ankyrin repeat homology
 C;Keywords: alternative splicing; cytoskeleton
 F;2-1880/Product: ankyrin 1, erythrocyte form 2 #status predicted <MAT>
 F;2-1513, 1676-1880/Product: ankyrin 2.2, erythrocyte #status predicted <MA2>
 F;44-76/Domain: ankyrin repeat homology <AN01>
 F;77-109/Domain: ankyrin repeat homology <AN02>
 F;110-142/Domain: ankyrin repeat homology <AN03>
 F;143-171/Domain: ankyrin repeat homology <AN04>
 F;172-204/Domain: ankyrin repeat homology <AN05>
 F;205-237/Domain: ankyrin repeat homology <AN06>
 F;238-270/Domain: ankyrin repeat homology <AN07>
 F;271-303/Domain: ankyrin repeat homology <AN08>
 F;304-336/Domain: ankyrin repeat homology <AN09>
 F;337-369/Domain: ankyrin repeat homology <AN10>
 F;370-402/Domain: ankyrin repeat homology <AN11>
 F;403-435/Domain: ankyrin repeat homology <AN12>
 F;436-468/Domain: ankyrin repeat homology <AN13>
 F;469-501/Domain: ankyrin repeat homology <AN14>
 F;502-534/Domain: ankyrin repeat homology <AN15>
 F;535-567/Domain: ankyrin repeat homology <AN16>
 F;568-600/Domain: ankyrin repeat homology <AN17>
 F;601-633/Domain: ankyrin repeat homology <AN18>
 F;634-666/Domain: ankyrin repeat homology <AN19>
 F;667-699/Domain: ankyrin repeat homology <AN20>
 F;700-732/Domain: ankyrin repeat homology <AN21>
 F;733-765/Domain: ankyrin repeat homology <AN22>
 F;766-798/Domain: ankyrin repeat homology <AN23>
 Query Match 13.6%; Score 182; DB 2; Length 1880;
 Best Local Similarity 26.4%; Pred. No. 4.2e-06;
 Matches 61; Conservative 34; Mismatches 135; Indels 1; Gaps 1;
 Qy 8 EDLIQTOQTASELGDPEPDGEEAADGSDTIVVLSLFPCTPEPVNPEDDASVSSPQAGSSL 67
 Db 421 KNLLQRGASPNSNVKVETPLHMAARAGHTEVAKYLLQNKAKVNAKDDQTPHLCAARI 480
 Qy 68 KHSTTLNRQRGNEVSALPATLDSLISIHQLAQGELDQLKEHLRKGDNLVNKPDERGFTP 127
 Db 481 GHTNMVKLLENNANPNLATAGHTPLHIAAREGHVETVALLKEASQACM-TKKGFTP 539
 Qy 128 LIWASAFGEIETVRFLEWGADPHILAKERESALSLASTGGYDIVGLLDERDVNDINYD 187
 Db 540 LHVAKYKGKVRVAELLERDAHPNAAGKNGLTPLHVAVHHNNLDIVKULLPRGGSPHSPA 599
 Qy 188 WNGGTPPLLYAVRGNHVKCVEALLARGADLTTEADSGYTPMDLAVALGYRKV 238
 Db 600 WNGGTPPLHYAKQNOVEVARSLLQYGGSSANAESVQGVTPHLAAQEGHAEM 650
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 Job time : 27 secs

